

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 17, 2005, 11:04:38 ; Search time 160 Seconds

(Without alignments)  
633,880 Million cell updates/sec

Title: US-09-826-212A-2

Perfect score: 1382  
Sequence: 1 MARPKTLKRVVIVAVILP.....YLCTIYGIYLVILVIV 259

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1382	100.0	259	9	US-09-826-212-2	Sequence 2, Appli
2	1382	100.0	259	9	US-09-887-879-1	Sequence 1, Appli
3	1382	100.0	259	9	US-09-992-964-1	Sequence 300, App
4	1382	100.0	259	14	US-10-028-072-300	Sequence 300, App
5	1382	100.0	259	14	US-10-140-808-300	Sequence 300, App
6	1382	100.0	259	14	US-10-121-049-300	Sequence 300, App
7	1382	100.0	259	14	US-10-123-904-300	Sequence 300, App
8	1382	100.0	259	14	US-10-140-470-300	Sequence 300, App
9	1382	100.0	259	14	US-10-175-746-300	Sequence 300, App
10	1382	100.0	259	14	US-10-176-918-300	Sequence 300, App
11	1382	100.0	259	14	US-10-176-921-300	Sequence 300, App

Result No.	Score	Match	Length	DB	ID	Description
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13	1382	100.0	259	14	US-10-140-474-300	Sequence 300, App
14	1382	100.0	259	14	US-10-142-431-300	Sequence 300, App
15	1382	100.0	259	14	US-10-143-114-300	Sequence 300, App
16	1382	100.0	259	14	US-10-142-419-300	Sequence 300, App
17	1382	100.0	259	14	US-10-123-262-300	Sequence 300, App
18	1382	100.0	259	14	US-10-142-423-300	Sequence 300, App
19	1382	100.0	259	14	US-10-121-050-300	Sequence 300, App
20	1382	100.0	259	14	US-10-141-755-300	Sequence 300, App
21	1382	100.0	259	14	US-10-143-032-300	Sequence 300, App
22	1382	100.0	259	14	US-10-123-108-300	Sequence 300, App
23	1382	100.0	259	14	US-10-123-236-300	Sequence 300, App
24	1382	100.0	259	14	US-10-123-261-300	Sequence 300, App
25	1382	100.0	259	14	US-10-140-921-300	Sequence 300, App
26	1382	100.0	259	14	US-10-140-928-300	Sequence 300, App
27	1382	100.0	259	14	US-10-121-045-300	Sequence 300, App
28	1382	100.0	259	14	US-10-123-292-300	Sequence 300, App
29	1382	100.0	259	14	US-10-123-903-300	Sequence 300, App
30	1382	100.0	259	14	US-10-124-819-300	Sequence 300, App
31	1382	100.0	259	14	US-10-124-822-300	Sequence 300, App
32	1382	100.0	259	14	US-10-140-925-300	Sequence 300, App
33	1382	100.0	259	14	US-10-160-498-300	Sequence 300, App
34	1382	100.0	259	14	US-10-124-824-300	Sequence 300, App
35	1382	100.0	259	14	US-10-127-825A-300	Sequence 300, App
36	1382	100.0	259	14	US-10-127-829A-300	Sequence 300, App
37	1382	100.0	259	14	US-10-127-835A-300	Sequence 300, App
38	1382	100.0	259	14	US-10-127-839A-300	Sequence 300, App
39	1382	100.0	259	14	US-10-127-901A-300	Sequence 300, App
40	1382	100.0	259	14	US-10-128-693A-300	Sequence 300, App
41	1382	100.0	259	14	US-10-131-813A-300	Sequence 300, App
42	1382	100.0	259	14	US-10-131-818A-300	Sequence 300, App
43	1382	100.0	259	14	US-10-131-823A-300	Sequence 300, App
44	1382	100.0	259	14	US-10-131-824A-300	Sequence 300, App
45	1382	100.0	259	14	US-10-131-830A-300	Sequence 300, App

#### ALIGNMENTS

RESULT 1  
US-09-826-212-2  
Sequence 2, Application US/09826212  
Patent No. US2001002156A1  
GENERAL INFORMATION:  
APPLICANT: Wei, Yang-Fei  
APPLICANT: Gentz, Reiner  
APPLICANT: Ruben, Steven  
APPLICANT: Ni, Jian  
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
FILE REFERENCE: 1488, 128006  
CURRENT APPLICATION NUMBER: US/09/826, 212  
CURRENT FILING DATE: 2001-04-05  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 259  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-826-212-2

Query Match 100.0%; Score 1382; DB 9; Length 259;  
Best Local Similarity 100.0%; Pred. No. 2, 1e-85;  
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1	1
MARPKTLKRVVIVAVILP	MARPKTLKRVVIVAVILP
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61	61
HTGACNPCEGVVYTNANNNRSCPCVCKSPDKKSSCTMTDVTVCCKEGSTFNNEN	HTGACNPCEGVVYTNANNNRSCPCVCKSPDKKSSCTMTDVTVCCKEGSTFNNEN
121	121
SPENCRCRSCPSGSEVVSNCSTMDIQCVBEFGANATVETPAABETMTNTSPGTPAPAAE	SPENCRCRSCPSGSEVVSNCSTMDIQCVBEFGANATVETPAABETMTNTSPGTPAPAAE
180	180

GenCore version 5.1.6  
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OM protein - protein search, using BW model

Run on: August 17, 2005, 10:58:37 ; Search time 23 Seconds  
(Without alignments)  
840.613 Million cell updates/sec

Title: US-09-826-212a-2

Perfect score: 1382  
Sequence: 1 MARIPRLKLVVVIVAVLVP.....YLSCRIIVGIIIVLIVLV 259

Scoring table: BLOSUM62

Gapop: 10.0, Gapext: 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
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5: /cgn2\_6/ptodata/1/1aa/6C.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/6D.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1382	100.0	259	4 US-09-573-986-2	Sequence 2, Appl1
3	1382	100.0	299	3 US-09-153-927-3	Sequence 3, Appl1
4	1382	100.0	299	4 US-09-114-618-4	Sequence 4, Appl1
5	1382	100.0	299	4 US-09-949-016-6422	Sequence 6, Appl1
6	1376	99.6	301	4 US-09-949-016-9189	Sequence 9189, Ap
7	634	45.9	386	4 US-09-086-483A-2	Sequence 2, Appl1
8	634	45.9	386	4 US-09-580-212-2	Sequence 2, Appl1
9	634	45.9	386	4 US-09-769-402-2	Sequence 2, Appl1
10	627	45.4	386	4 US-09-130-491-6	Sequence 6, Appl1
11	480	34.7	452	4 US-09-949-016-9855	Sequence 9855, Ap
12	472	34.2	234	4 US-09-130-491-12	Sequence 12, Appl1
13	472	34.2	467	4 US-09-086-483A-6	Sequence 6, Appl1
14	472	34.2	467	4 US-09-580-212-6	Sequence 6, Appl1
15	472	34.2	467	4 US-09-769-402-6	Sequence 6, Appl1
16	472	34.2	468	4 US-09-013-895A-2	Sequence 2, Appl1
17	472	34.2	468	4 US-09-565-918-2	Sequence 2, Appl1
18	472	34.2	468	4 US-09-448-868-2	Sequence 2, Appl1
19	472	34.2	468	4 US-09-949-016-6423	Sequence 6, Appl1
20	452	32.7	350	4 US-09-134-618-6	Sequence 6, Appl1
21	448	32.4	440	4 US-09-536-201-2	Sequence 2, Appl1
22	448	32.4	440	4 US-09-578-392-2	Sequence 2, Appl1
23	448	32.4	440	4 US-09-578-392-2	Sequence 2, Appl1
24	398.5	28.8	424	3 US-09-333-593A-8	Sequence 8, Appl1
25	380.5	27.7	411	3 US-09-134-618-2	Sequence 2, Appl1
26	379.5	27.5	412	3 US-09-333-593A-2	Sequence 2, Appl1
27	379.5	27.5	411	3 US-09-329-633A-2	Sequence 2, Appl1

28	379.5	27.5	411	3 US-09-079-029-1	Sequence 1, Appl1
29	379.5	27.5	411	4 US-09-874-138-2	Sequence 2, Appl1
30	236.5	17.1	303	3 US-09-333-593A-4	Sequence 4, Appl1
31	212	15.3	368	2 US-08-651-579-2	Sequence 2, Appl1
32	201.5	14.6	427	3 US-09-086-483A-4	Sequence 4, Appl1
33	201.5	14.6	427	3 US-09-041-886-2	Sequence 2, Appl1
34	201.5	14.6	427	3 US-09-006-353A-5	Sequence 5, Appl1
35	201.5	14.6	427	4 US-09-573-986-5	Sequence 5, Appl1
36	201.5	14.6	427	4 US-09-769-402-4	Sequence 4, Appl1
37	201.5	14.6	427	4 US-09-769-402-4	Sequence 4, Appl1
38	201.5	14.6	427	4 US-09-748-537-13	Sequence 13, Appl1
39	201.5	14.6	427	4 US-09-949-016-6233	Sequence 24, Appl1
40	201.5	14.6	427	4 US-09-949-016-6233	Sequence 6233, Ap
41	201.5	14.6	455	3 US-09-527-236A-4	Sequence 4, Appl1
42	201.5	14.6	455	3 US-09-756-854-4	Sequence 4, Appl1
43	201.5	14.6	464	4 US-09-949-016-9441	Sequence 9441, Ap
44	200.5	14.5	425	4 US-09-748-537-14	Sequence 14, Appl1
45	198	14.3	398	4 US-09-612-033B-14	Sequence 14, Appl1

## ALIGNMENTS

RESULT 1  
US-09-006-353A-2  
Sequence 2, Application US/09006353A

Patent No. 6261801

GENERAL INFORMATION:

APPLICANT: WEI, YING-PEI

APPLICANT: GENTZ, REINER

APPLICANT: RUBEN, STEVEN

TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/006,353A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKS, ANDERS A

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF311

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 259 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: protein

US-09-006-353A-2

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Best Local Similarity 100.0%; Pred. No. 1,4e-101;  
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1 MARIPRLKLVVVIVAVLVP...AYATTAARKEEVPQQTVAPOOORHSFKGBECFAGSHRS 60

GenCore version 5.1.6  
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OM nucleic - nucleic search, using BW model

Run on: August 19, 2005, 06:54:16 ; Search time 988 Seconds  
(without alignments)  
9153.554 Million cell updates/sec

Title: US-09-826-212A-1

Perfect score: 1392  
Sequence: 1 cctctccacgcgcagcaact.....agatttcctcgtaaaaaa 1392

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	1103	79.2	1180	9	US-09-887-879-2
5	1103	79.2	1180	9	US-09-887-879-4
6	1103	79.2	1180	9	US-09-982-964-2
7	1103	79.2	1180	9	US-09-982-964-4

8	1103	79.2	1180	15	US-10-242-383-2	Sequence 2, Appl1
9	1103	79.2	1180	15	US-10-242-383-4	Sequence 4, Appl1
10	1092	78.4	1102	14	US-10-028-072-299	Sequence 299, App
11	1092	78.4	1102	14	US-10-140-808-299	Sequence 299, App
12	1092	78.4	1102	14	US-10-121-049-299	Sequence 299, App
13	1092	78.4	1102	14	US-10-123-904-299	Sequence 299, App
14	1092	78.4	1102	14	US-10-140-470-299	Sequence 299, App
15	1092	78.4	1102	14	US-10-175-746-299	Sequence 299, App
16	1092	78.4	1102	14	US-10-175-746-299	Sequence 299, App
17	1092	78.4	1102	14	US-10-175-746-299	Sequence 299, App
18	1092	78.4	1102	14	US-10-175-746-299	Sequence 299, App
19	1092	78.4	1102	14	US-10-143-431-299	Sequence 299, App
20	1092	78.4	1102	14	US-10-143-431-299	Sequence 299, App
21	1092	78.4	1102	14	US-10-142-423-299	Sequence 299, App
22	1092	78.4	1102	14	US-10-142-423-299	Sequence 299, App
23	1092	78.4	1102	14	US-10-142-423-299	Sequence 299, App
24	1092	78.4	1102	14	US-10-142-423-299	Sequence 299, App
25	1092	78.4	1102	14	US-10-142-423-299	Sequence 299, App
26	1092	78.4	1102	14	US-10-141-050-299	Sequence 299, App
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28	1092	78.4	1102	14	US-10-141-050-299	Sequence 299, App
29	1092	78.4	1102	14	US-10-123-108-299	Sequence 299, App
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37	1092	78.4	1102	14	US-10-123-108-299	Sequence 299, App
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40	1092	78.4	1102	14	US-10-123-108-299	Sequence 299, App
41	1092	78.4	1102	14	US-10-123-108-299	Sequence 299, App
42	1092	78.4	1102	14	US-10-123-108-299	Sequence 299, App
43	1092	78.4	1102	14	US-10-123-108-299	Sequence 299, App
44	1092	78.4	1102	14	US-10-123-108-299	Sequence 299, App
45	1092	78.4	1102	14	US-10-123-108-299	Sequence 299, App

#### ALIGNMENTS

RESULT 1

US-09-826-212-1

Sequence 1, Application US/09826212

Patent No. US20010021516A1

GENERAL INFORMATION:

APPLICANT: Wei, Ying-Fel

APPLICANT: Genetz, Reiner

APPLICANT: Ruben, Steven

APPLICANT: N. J. J. J.

TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5

FILE REFERENCE: 1488.1280006

CURRENT APPLICATION NUMBER: US/09/826.212

CURRENT FILING DATE: 2001-04-05

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patent in version 3.0

SEQ ID NO 1

LENGTH: 1392

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS (959)

NAME/KEY: mat.peptide

NAME/KEY: (261)...

NAME/KEY: sig.peptide

NAME/KEY: (183)...

NAME/KEY: (260)

Query Match: 100.0%; Score 1392; DB 9; Length 1392;

Best Local Similarity: 100.0%; Pred. No. 0;

NAME/KEY: mat\_peptide

Sequence 1, April  
Sequence 1, April  
Sequence 1, April  
Sequence 1, April  
Sequence 1, April  
Sequence 1, April  
Sequence 16, April  
Sequence 16, April  
Sequence 28818, A  
Sequence -119433  
Sequence -12264, A  
Sequence -15726, A  
Sequence 1, April  
Sequence 2, April  
Sequence 1, April  
Sequence 1, April  
Sequence 1, April